Evidence suggests that the SARS-CoV-2 Spike (S) protein may target coiled-coil regions of numerous cytoskeletal and cytoskeleton-associated proteins

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ABSTRACT

Understanding the interactions between host and viral envelope proteins is essential to get insights into the dynamics of viral infection. To investigate more closely the mechanisms governing SARS-CoV-2 entry and intracellular trafficking, we reanalyzed the most extensive SARS-CoV-2–human protein–protein interactome dataset currently available. Our investigation centered on the Spike S protein, a key player in initiating viral infection by binding to the host cell membrane receptor Angiotensin-Converting Enzyme 2 (ACE2). We first present evidence demonstrating the statistical overrepresentation of actin-binding proteins among the Spike S partners/interactors. Next, we show that a majority of these partners contains a structural domain sharing high similarity with the C-terminal region of the Myosin II heavy chain, Myosin II being known for its roles in muscle contraction and various cellular motility processes. We subsequently demonstrate that this domain is particularly prevalent in actin-binding proteins, Intermediate Filaments proteins and Kinesins, which all are related to the cytoskeleton known to be involved in diverse cellular functions, including endocytosis and intracellular transport — processes crucial for viral infections. Finally, we highlight that the structural domain mentioned above is a bonafide coiled-coil region. We therefore conclude that Spike S might target proteins possessing such regions. These results align well with our previous findings, which suggested that the C-terminal portion of the Spike S protein shares similarities with the human protein prominin-1/CD133. Notably, CD133 is specifically located on the apical surface of cells and is associated with microvilli, structures characterized by a dense core of cross-linked actin filaments. Collectively, our findings suggest that the interactions between SARS-CoV-2 Spike S and human proteins, potentially mediated by coiled-coil regions, may have been underestimated. This opens up new avenues of research to elucidate the mechanisms underlying SARS-CoV-2 entry and intracellular trafficking.

Keywords: SARS-CoV-2–human protein–protein interactome, Protein Structure Prediction, Phyre2, BackPhyre, Bioinformatics

Introduction

Exploring protein-protein interactions (PPI) between host proteins and viral proteins has emerged as a relevant approach in viral infection research (Calderwood *et al.*, 2007). In the context of COVID-19, such approaches have been used to identify pharmacological agents with antiviral activity or potential host therapeutic targets (Gordon *et al.*, 2020, Zhou *et al.*, 2022). In this study, we focused on the most comprehensive and reliable SARS-CoV-2–human PPI data available to date (Zhou *et al.*, 2022), based on both two-hybrid (Y2H) and affinity purification-mass spectrometry (AP-MS), to enhance our understanding of virus infection dynamics (encompassing entry and propagation both intra- and extracellularly).

Large-scale protein interaction studies using techniques like Y2H (Rajagopala *et al.*, 2015) and AP-MS (Causier *et al.*, 2004) have well-documented limitations. For example, they might miss transient interactions or detect interactions between proteins that are not normally found in the same cellular compartment or not expressed at the same time in the cell, *etc.* (EBI Training Online Courses, (Millan, 2022)). Despite these weaknesses, however, Y2H and AP-MS often generate high-quality data which can be used as a reliable and robust basis for further investigation. In our context, at first glance, this assertion might seem surprising given a well-known major limitation of the aforementioned interactome: the critical interaction between the Spike S binding domain (RBD) and the host Angiotensin-Converting Enzyme 2 (ACE2), which allows for the initiation of viral infection, has not been identified. However, while this latter interaction is clearly of great importance, this interactome can potentially help to detect or reveal other types of interesting and meaningful interactions, such as those involving other regions of Spike S, or those taking place at other stages of the infection process.

Relying on the Spike S sub-network of the aforementioned interactome, we first demonstrate that actin-binding proteins are statistically overrepresented within the set of Spike S interactors/partners. Using Phyre2 (Kelley *et al.*, 2015), a popular bioinformatics method for protein structure prediction, we reveal that a majority of Spike S partners contain a structural domain sharing similarities with the C-terminal part of the Myosin II heavy chain. Next, using BackPhyre, a tool that identifies proteins harboring a given structural domain, we identified a set of human proteins containing this domain with high probability. Subsequently, we show that this set of proteins is particularly abundant in human cytoskeletal and associated proteins (and statistically overrepresented in actin-binding proteins, Intermediate Filaments proteins and kinesins), as well as in proteins involved in microtubule dynamics, all essential for processes such as vesicle transport, mitosis, and cilia/flagella movement. Given the well-established coiled-coil structure of the C-terminal domain of the Myosin II heavy chain, we infer that Spike S might target proteins containing such regions (an overall view of our results is given in the Figure at the end of the paper).

Material and methods

Interactome data

The interactions between the Spike S protein and human proteins used in this paper are extracted from a protein-protein interactome published in Nature Biotechnology (Zhou et al., 2022). They involved 22 human proteins, hereafter denoted as interactors or partners, as shown in Table 1 below.

Table 1 - Each line represents a Spike S partner. The 'UniProtID' column identifies the protein using its unique identifier in the UniProt database. The 'Protein Name' column indicates the name of the protein. The 'Technique of identification' column refers to the approach used to identify the considered interaction, where 'Y2H' denotes/stands for 'Yeast Two-Hybrid' and 'AP-MS' stands for 'Affinity Purification-Mass Spectrometry'.

UniProt ID	Protein Name	Technique of identification
ACTN4_HUMAN	Alpha-actinin-4	Y2H
MYH9_HUMAN	Myosin-9	AP-MS
MYH10_HUMAN	Myosin-10	AP-MS
MYH14_HUMAN	Myosin-14	AP-MS
TPM1_HUMAN	Tropomyosin alpha-1 chain	AP-MS
TPM2_HUMAN	Tropomyosin beta chain	AP-MS
TPM3_HUMAN	Tropomyosin alpha-3 chain	AP-MS
TPM4_HUMAN	Tropomyosin alpha-4	AP-MS
COR1C_HUMAN	Coronin-1C	AP-MS
TMOD3_HUMAN	Tropomodulin-3	AP-MS
BICL2_HUMAN	BICD family-like cargo adapter 2	Y2H
CYTSA_HUMAN	Cytospin-A	AP-MS
EPIPL_HUMAN	Epiplakin	AP-MS
ITBP2_HUMAN	Integrin beta-1-binding protein 2	Y2H
LZTS2_HUMAN	Leucine zipper putative tumor suppressor 2	Y2H
LMO7_HUMAN	LIM domain only protein 7	AP-MS
ML12B_HUMAN	Myosin regulatory light chain 12B	AP-MS
MYL9_HUMAN	Myosin regulatory light polypeptide 9	AP-MS
MYL6B_HUMAN	Myosin light chain 6B 208	AP-MS
MYL6_HUMAN	Myosin light polypeptide 6	AP-MS
PARP1_HUMAN	Poly(ADP-ribose) polymerase 1	AP-MS
STON2_HUMAN	Stonin 2905	AP-MS;Y2H

Protein structure prediction, Identification of proteins containing a given structural domain

Phyre2 (Protein Homology/AnalogY Recognition Engine), a free web-based service for protein structure prediction, has been used for protein modeling (*i.e.*, inferring the three-dimensional structure of a protein from its amino acid sequence) ; BackPhyre has been utilized to identify proteins containing a given structural domain (Kelley *et al.*, 2015).

Protein Data Bank entry 6XE9

Structure 6XE9 (https://www.rcsb.org/structure/6XE9) represents the heavy chain of Myosin II complex (Yang *et al.*, 2020) of *Meleagris gallopavo* (wild turkey). Its UniProt accession number is G1N5L2 and its sequence length is 1979 amino acids. This protein, also referred to as "class II myosin heavy chain," is a part of the "myosin II complex" which enables muscle cells to contract and facilitates movement and shape changes in non-muscle cells. This complex contains two class II myosin heavy chains, two myosin essential light chains, and two myosin regulatory light chains. These chains assemble to form an alpha-helical, coiled-coil tail.

G1N5L2 is not fully modeled; the protein segments 1-23, 205-210, 635-655, 955-1396, and 1676-1979 are missing. As a consequence:

- Protein segment 24-204 aligns with structure segment 1-181.
- Protein segment 211-634 aligns with structure segment 182-605.
- Protein segment 656-954 aligns with structure segment 606-904.
- Protein segment 1397-1675 aligns with structure segment 905-1183.

G1N5L2 is made of two InterPro domains: a Myosin Head Motor Domain (IPR001609, positions 78-790) and a Myosin Tail Domain (IPR002928, positions 854-1934). The alignments between the Myosin Head domain and the modeled part of this domain are the following:

- Protein segment 78-204 aligns with structure segment 55-181,
- Protein segment 211-634 aligns with structure segment 182-605,
- Protein segment 656-790 aligns with structure segment 606-740.

The alignments between the Myosin Tail domain and the modeled part of this domain are the following:

- Protein segment 854-954 aligns with structure segments 804-904.
- Protein segment 1397-1675 aligns with structure segments 905-1183.

Thus, the modeled Myosin Head covers structure segment 55-740, and the modeled Myosin Tail spans structure segment 804-1183.

Statistical analysis tool

Fisher's exact test was conducted on the website BiostatTGV (https://biostatgv.sentiweb.fr/?module=tests/fisher).

Results

Spike S partners are enriched in cytoskeleton-associated proteins, particularly actin-binding proteins

Among the 22 Spike S partners (see Table 2 for a summary), 10 are annotated as "Actin Binding Proteins" according to a study which gathered a collection of 418 actin-associated proteins (AAPs) whose direct interactions with actin have been experimentally verified (Gao & Nakamura, 2022). These 10 proteins play various roles in actin dynamics (see UniProt annotations (UniProt Consortium, 2025), (Gao & Nakamura, 2022) and (Cooper, 2000)):

- "Alpha-actinin-4" (UniProt ID ACTN4_HUMAN) is a component of the actin cytoskeleton.

- "Myosin-9" (UniProt ID MYH9_HUMAN), "Myosin-10" (MYH10_HUMAN), and "Myosin-14" (MYH14_HUMAN) are cellular myosin.

- "Tropomyosin alpha-1 chain" (UniProt ID TPM1_HUMAN), "Tropomyosin beta chain" (TPM2_HUMAN), "Tropomyosin alpha-3 chain" (TPM3_HUMAN), and "Tropomyosin alpha-4 chain" (TPM4_HUMAN) are involved in stabilizing actin filaments (e.g., protecting F-actin from severing).

- "Coronin-1C" (UniProt ID COR1C_HUMAN) and "Tropomodulin-3" (TMOD3_HUMAN) are involved in stabilizing, bundling, and capping actin, respectively.

In the 'Statistical Analysis' section, we demonstrate a statistically significant enrichment of actin-binding proteins among the set of Spike S protein interactors compared to their expected distribution within the human proteome.

The remaining 12 Spike S partners interact directly or indirectly with the cytoskeleton, an intricate network of filaments within cells comprising actin filaments (AFs), microtubules (MTs), and intermediate filaments (IFs) (Cooper, 2000):

- "BICD family-like cargo adapter 2" (UniProt ID BICL2_HUMAN) belongs to the BICD family-like. "BICD family-like cargo adapter 1" (BICL1_HUMAN), a member of this family, is predicted to

connect the dynein motor complex to various cargos and enhance dynein's ability to move along microtubules (MTs) for extended distances without falling off (see UniProt annotations).

- "Cytospin-A" (UniProt ID CYTSA_HUMAN) is documented as a "cross-linking" protein that functionally interacts with both the actin cytoskeleton and MTs (Saadi *et al.*, 2011).

- "Epiplakin" (UniProt ID EPIPL_HUMAN) is a cytoskeletal linker protein that connects to IFs and controls their reorganization in response to stress ((Jang *et al.*, 2005), (Shimada *et al.*, 2013), (Kokado *et al.*, 2016)).

- "Integrin beta-1-binding protein 2" (UniProt ID ITBP2_HUMAN), also referred as Melusin, is a muscle-specific interactor for the beta(1) integrin's cytoplasmic domain, which interacts with the actin-binding protein alpha-actinin (Otey *et al.*, 1990)

- "Leucine zipper putative tumor suppressor 2" (UniProt ID LZTS2_HUMAN) is a beta-catenin-interacting protein that modulates beta-catenin signaling and localization (Thyssen *et al.*, 2006). Beta-catenin, a crucial regulator of cell-cell adhesion, forms a complex with alpha-catenin that bridges cadherins (adherens junction components) and the actin cytoskeleton (Kobielak & Elaine Fuchs, 2004).

- "LIM domain only protein 7" (UniProt ID LMO7_HUMAN) belongs to a group of proteins that bind to stressed actin filaments (Winkelman *et al.*, 2020).

- "Myosin regulatory light chain 12B" (UniProt ID ML12B_HUMAN) and "Myosin regulatory light polypeptide 9" (MYL9_HUMAN) are part of the Myosin II complex, as are "myosin light chain 6B" (MYL6B_HUMAN) and "myosin light polypeptide 6" (MYL6_HUMAN). These light chains do not bind to actin but interact with the myosin heavy chain, which allow Myosin II complex to bind to actin.

- "Poly(ADP-ribose) polymerase 1" (UniProt ID PARP1_HUMAN), which is mainly and well documented to play a key role in DNA repair, also interacts with Transgelin, an actin-binding protein, in human colon cancer cells (Lew *et al.*, 2020). Note that several studies underscore the functional importance of lamins, actin, myosin, spectrin, and the linker of nucleoskeleton and cytoskeleton (LINC) complex in DNA repair (Lambert, 2019). Finally note that while PARP1 is involved in multiple antiviral mechanisms, several viruses can inhibit these antiviral functions and recruit and utilize PARP1 for their own benefit (Sobotka & Tempera, 2024).

- "Stonin 2" is an adaptor protein that interacts with components of the endocytic machinery (Martina *et al.*, 2020), which are involved in regulating coat assembly, vesicle budding, and signal transduction pathways along with the actin cytoskeleton (Chakrabarti *et al.*, 2021).

In conclusion, the set of 22 Spike S partners is enriched in "cytoskeleton-associated proteins", particularly in actin-binding proteins which are statistically over-represented.

Table 2 - Each line represents a Spike S partner. The 'UniProtID' column identifies the protein using its unique identifier in the UniProt database. The 'Protein Name' column indicates the name of the protein. The 'Length (AA)' column indicates the total length of the protein sequence (in amino acids). The 'Link with Cytoskeleton' column indicates whether a documented link exists between the considered Spike S partner and the cytoskeleton. The 'Similarities with the C-terminal part of Myosin II heavy chain (PDB entry 6XE9)' column indicates whether the considered Spike S partner shares similarities (+) or does not share similarities (-) with the C-terminal tail of the Myosin II heavy chain (this latter column refers to subsection 'A majority of Spike S partners share similarities with the C-terminal myosin II heavy chain domain').

UniProt ID	Protein Name	Length (AA)	Link with Cytoskeleton	Similarities with the C-terminal part of the Myosin II heavy chain (PDB entry 6XE9)
ACTN4_HUMAN	Alpha-actinin-4	911	actin-binding	+
MYH9_HUMAN	Myosin-9	1960	actin-binding	+
MYH10_HUMAN	Myosin-10	1976	actin-binding	+
MYH14_HUMAN	Myosin-14	1995	actin-binding	+
TPM1_HUMAN	Tropomyosin alpha-1 chain	284	actin-binding	+
TPM2_HUMAN	Tropomyosin beta chain	284	actin-binding	+
TPM3_HUMAN	Tropomyosin alpha-3 chain	285	actin-binding	+
TPM4_HUMAN	Tropomyosin alpha-4	248	actin-binding	+
COR1C_HUMAN	Coronin-1C	474	actin-binding	-
TMOD3_HUMAN	Tropomodulin-3	352	actin-binding	-
BICL2_HUMAN	BICD family-like cargo adapter 2	508	connects the dynein motor complex to various cargos and enhances dynein's ability to move along microtubules	+
CYTSA_HUMAN	Cytospin-A	1117	interacts with both the actin cytoskeleton and microtubules	+
EPIPL_HUMAN	Epiplakin	5088	cytoskeletal linker protein that connects to Intermediate Filaments	-
ITBP2_HUMAN	Integrin beta-1-binding protein 2	347	Interacts with alpha-actinin	-
LZTS2_HUMAN	Leucine zipper putative tumor suppressor 2	669	forms a complex with alpha-catenin that bridges cadherins (adherens junction components) and the actin cytoskeleton	+
LMO7_HUMAN	LIM domain only protein 7	1683	binds to stressed Actin Filaments	+
ML12B_HUMAN	Myosin regulatory light chain 12B	172	myosin regulatory subunit	-
MYL9_HUMAN	Myosin regulatory light polypeptide 9	172	myosin regulatory subunit	-
MYL6B_HUMAN	Myosin light chain 6B 208	208	regulatory light chain of Myosin	-
MYL6_HUMAN	Myosin light polypeptide 6	151	regulatory light chain of Myosin	-
PARP1_HUMAN	Poly(ADP-ribose) polymerase 1	1014	not really linked although it has been shown to interact with Transgelin, an actin-binding protein, in human colon cancer cells	-
STON2_HUMAN	Stonin 2905	905	interacts with components of the endocytic machinery - actin assembly being an essential element of endocytosis	-

A majority of Spike S partners share similarities with the C-terminal Myosin II heavy chain domain

The observation that a protein interacts with a set of proteins often leads to the speculation that these proteins share a common domain mediating the identified interactions. This is why we investigated whether a majority of the 22 Spike S protein partners would share a common domain. Using InterPro domain annotations, we found no such domain. Therefore, we decided to use Phyre2, a protein 3D structure prediction method (Kelley *et al.*, 2015), to address this question.

We ran Phyre2 on each of the 22 Spike S partners (see Supplemental file 1). Interestingly, a careful manual examination of the results revealed that 12 out of the 22 Spike S partners shared a high-confidence similarities with the C-terminal part of the PDB entry 6XE9, *i.e.*, the myosin II heavy chain of the myosin II complex of *Meleagris gallopavo* (wild turkey) (see Material and Methods section 'Protein Data Bank entry 6XE9' for a detailed presentation of 6XE9). Its UniProt accession number is G1N5L2 and its sequence length is 1979 amino acids (see (Yang *et al.*, 2020)). It is made of two InterPro domains: a Myosin Head Motor Domain (IPR001609, positions 78-790) and a Myosin Tail Domain (IPR002928, positions 854-1934). As highlighted in subsection 'Protein Data Bank entry 6XE9', 6XE9 is not fully modeled. Specifically, the modeled Myosin Head covers structure segments 55-740, and the modeled Myosin Tail spans structure segments 804-1183.

The 12 Spike S partners that share similarities with the C terminal part of the PDB entry 6XE9 are listed in the Table 3 below. For each of these latter, this table summarizes some protein characteristics (UniProt ID, name, length) as well as its alignment with PDB entry 6XE9 and Phyre2's confidence score.

The results reveal a clear fit between protein structure 6XE9 and myosin heavy chains MYH9, 10, and 14, which is consistent as these proteins belong to the same family. The tropomyosins (TPM1, 2, 3, and 4) exhibit a significant fit with the tail of 6XE9, leaving only a minor portion of their sequences not covered. A substantial portion of the actin sequence ACTN4 also aligns with 6XE9 tail. Finally, the similarity shared between 6XE9 and BICL2 (resp., CYSTA, LMO7, and LZTS2) is localized in the tail region of 6XE9. In conclusion, these 12 proteins share similarities with the Myosin tail domain of 6XE9.

Table 3 - Each line represents a Spike S partner exhibiting similarities with the C-terminal part of PDB entry 6XE9 (Myosin II heavy chain). The 'ID' column provides the protein's UniProt identifier. The 'Length' column indicates the protein's length (in amino acids). The 'Query/6XE9' column shows the aligned amino acid positions between the query protein and the reference structure (6XE9), in the format start-end (query)/start-end (6XE9). The 'Confidence' column displays the Phyre2 confidence score for the similarity, indicating the probability of accurate alignment.

ID	Length	Query / 6XE9	Confidence
ACTN4	911	299-758 / 736-1183	98.44
BICL2	508	30-463 / 793-1182	98.65
CYTSA	1117	341-800 / 730-1183	98.91
LMO7	1683	714-1096 / 803-1183	97.05
LZTS2	669	331-663 / 853-1182	99.58
MYH9	1960	23-1223 / 3-1183	100.00
MYH10	1976	26-1230 / 2-1183	100.00
MYH14	1995	47-1247 / 3-1183	100.00
TPM1	284	1-282 / 810-1091	99.74
TPM2	284	1-282 / 810-1091	99.72
TPM3	285	2-284 / 810-1092	99.74
TPM4	248	4-243 / 828-1067	99.26

The set of human proteins identified by BackPhyre is enriched in cytoskeletal-associated proteins, including actin-binding proteins, intermediate filament proteins, and kinesins

To identify potential human interactors/partners of Spike S, we employed BackPhyre, often called 'Phyre2 in reverse' (see BackPhyre documentation). Given a 3D structure, BackPhyre determines if this structure (or part of this structure) is present in proteins of a genome/proteome of interest. We queried the human proteome (NCBI Reference Sequence database) using PDB structure 6XE9 (the heavy chain of myosin II complex). BackPhyre returned 999 protein entries

with probabilities ranging from 95.8% to 100%. According to BackPhyre's documentation, if a match probability exceeds 90%, one can generally be very confident that the protein adopts the overall fold shown and that the core of the protein is modelled at high accuracy (2-4Å rmsd from native, true structure).

From the original 999 entries, we excluded 195 sequences prefixed with "XP_," indicating they were not curated RefSeq records. This left us with a set of 804 curated protein sequences (starting with "NP_"). We then grouped together the different isoforms of each protein-coding gene, resulting in 622 distinct protein clusters (see Supplemental file 2).

Given that we fed BackPhyre with the entire PDB structure 6XE9, and to the extent that the feature identified as common to 12 out of the 22 Spike S' partners (see Results) concerns the C-terminal part of 6XE9, we performed a filtering step to preserve clusters that encompass at least one isoform possessing this characteristic. To achieve this, we identified the boundaries of the largest motif of 6XE9 common to all of our 12 previously referred proteins; we found 853-1067. This step narrowed down the set to 488 protein clusters. Finally, to represent each protein cluster uniquely, we selected a single isoform from those with multiple isoforms.

We then aimed to group together proteins sharing similar features. Although some proteins might obviously belong to multiple clusters, for the sake of clarity, we opted for a definitive assignment to a single cluster within this analysis (see Supplemental file 3).

The creation of the first three clusters was driven by our analysis of the 22 SARS-CoV-2 Spike S partners, which identified an enrichment of both actin-binding proteins and proteins associated with the cytoskeleton (Actin Filaments, Intermediate Filaments, and Microtubules). These trends were confirmed by a quick look at the 488 proteins identified previously (Note that this set of proteins is referred to as the ‘focus set’ in the ‘Discussion’ section of this paper).

1./ ‘Link To Actin’ cluster:

We relied on a list of manually curated Actin-Associated Proteins (AAPs) (Gao & Nakamura, 2022), which contain Actin-Binding Proteins (ABPs), to identify the actin-binding proteins of our set. This resulted in a cluster that includes proteins known to interact with actin, such as actin, myosin, and tropomyosin. Additionally, we also included proteins functionally linked to actin but not explicitly annotated as actin-binding proteins. The 'Link To Actin' cluster contains 67 proteins, among which 56 are ABPs; we demonstrate (see ‘Statistical analysis’) that our set of 488 proteins is statistically enriched with ABPs compared to their distribution in the human proteome.

2./ ‘Link to Intermediate Filaments’ cluster:

We relied on UniProt annotations to identify Intermediate Filament (IF) proteins within the human proteome. (query: "(proteome:UP000005640) AND (go:0005882) where ‘0005882’ refers to ‘intermediate filament’ in Gene Ontology). 'Link to Intermediate Filaments' cluster groups together IFs, such as keratins, vimentin, neurofilament proteins, etc., along with proteins linked to intermediate filaments. 'Link to Intermediate Filaments' contains 71 proteins among which 68 are IFs. We show in ‘Statistical analysis’ that our set of 488 proteins is statistically enriched with IFs compared to their distribution in the human proteome.

3./ ‘Link To Kinesin and Dynein’ cluster:

Our analysis of our set of 488 proteins revealed an absence of tubulins, the building blocks of microtubules. Despite this, we identified several kinesin and dynein motor proteins, known for their interaction with microtubules to facilitate intracellular transport of various cargo like vesicles,

organelles, and chromosomes. We additionally put four 'Tektins' in this cluster. According to UniProt annotations, these latter are microtubule inner proteins (MIPs) that are components of the dynein-decorated doublet microtubules (DMTs) in cilia and flagellar axonemes. The 'Link To Kinesin and Dynein' cluster contains 46 proteins, among which 24 are kinesins (query: "(proteome:UP000005640) AND (go:0005871)" where ‘0005871’ refers to ‘kinesin complex’ in Gene Ontology). We prove in section ‘Statistical analysis’ that our set of 488 proteins is statistically enriched with kinesins compared to their distribution in the human proteome.

4./ ‘Link To Microtubule’ cluster:

The identification of microtubule motor proteins (kinesins and dyneins, as shown in the cluster above) prompted us to search for microtubule-related proteins in our set of 488 proteins. Microtubules, anchored at the centrosome (the MTOC), extend towards the cell periphery and play a vital role in various cellular processes, e.g., during mitosis, they reorganize into the mitotic spindle, ensuring proper chromosome segregation. Additionally, cilia and flagella are microtubule-based structures that contribute to cellular functions. Not surprisingly, our analysis identified many proteins associated with these structures (centrosome, mitotic spindle, cilia, and flagella). These proteins were subsequently grouped together into 5 different subclusters, namely, ‘Link to MT', Link To Centrosome', 'Link To Cilia', 'Link To “Sperm Flagellar"’, and 'Link To Spindle'. The 'Link To Microtubule' cluster contains 104 proteins.

5./ ‘Link To Trafficking’ cluster:

Functional analysis of the remaining proteins allowed us to identify an enrichment in proteins associated with transport and trafficking pathways. The 'Link To Trafficking' cluster contains 51 proteins, among which are several members of the BICD family. Members of this family are known to link the dynein motor complex to various cargos.

6. 'Various' cluster:

We next identified several clusters with a moderate number of proteins, associated for instance with 'defense' or 'LINC (Linker of Nucleoskeleton and Cytoskeleton)', this latter grouping 3 proteins involved in the connection between the nuclear lamina and the cytoskeleton. The 'Various' cluster contains 106 proteins.

7. 'Lacking UniProt Summary' cluster:

This cluster contains 43 proteins lacking a UniProt 'Function' field, which was one of our main source of information for performing our clustering.

WARNING: While conceived as a kind of counterpart to Phyre2, BackPhyre's results may not always perfectly align with Phyre2's. This means that BackPhyre might identify a human protein with similarities to the input 3D structure, while Phyre2 may not find any or identify different similarties. In our case, these discrepancies can be primarily attributed to the different release dates of the genomes/proteomes used for searching. These databases are not updated regularly due to the huge computational resources required to process each protein sequence and build its associated Hidden Markov Model (HMM).

Statistical analysis

Actin-binding proteins are statistically overrepresented among the 22 Spike S protein partners

To evaluate whether the set of 22 Spike S partners is enriched with actin-binding proteins, we performed a Fisher's exact test. We tested the null hypothesis that the 10 actin-binding proteins

within this set are a random sample from the distribution of actin-binding proteins in the human proteome. To determine the human actin-binding proteins, we relied on a collection of 418 actin-associated proteins (AAPs) whose direct interactions with actin have been experimentally verified, as provided in (Gao & Nakamura, 2022). According to UniProt (UniProt Consortium, 2024), the human proteome comprises approximately 82518 proteins (query: (proteome:UP000005640)). The contingency table is thus as follows:

	Observed count	Expected count
Actin binding	10	(418/82518)*22
Not actin binding	12	((82518-418)/82518)*22

That is to say:

	Observed count	Expected count
Actin binding	10	0
Not actin binding	12	22

The calculated Fisher's exact p-value is 0.000521 (see Material and Methods). Given a significance level of 0.05, we reject the null hypothesis and conclude that the actin-binding proteins in our set of 22 proteins are significantly overrepresented compared to their distribution in the human proteome.

Actin-binding proteins are statistically overrepresented among human proteins identified by BackPhyre as having similarities to the C-terminal domain of Myosin II heavy chain

To evaluate whether the set of 488 proteins identified by BackPhyre is enriched with actin-binding proteins, we performed a Fisher's exact test. We tested the null hypothesis that the 56 actin-binding proteins within this set are a random sample from the distribution of actin-binding proteins in the human proteome. To determine the human actin-binding proteins, we relied on a collection of 418 actin-associated proteins (AAPs) whose direct interactions with actin have been experimentally verified, as provided in (Gao & Nakamura, 2022). According to UniProt (UniProt Consortium, 2024), the number of proteins expressed by humans is 82518 (query: (proteome:UP000005640)). The contingency table is thus as follows:

	Observed count	Expected count
Actin binding	56	(418/82518)*488
Not actin binding	432	((82518-418)/82518)*488

That is to say:

	Observed count	Expected count
Actin binding	56	3
Not actin binding	432	485

The calculated Fisher's exact p-value is 1.3074430605672E-14 (see Material and Methods). Given a significance level of 0.05, we reject the null hypothesis and conclude that actin-binding proteins are significantly overrepresented within the set of 488 proteins identified by BackPhyre compared to their expected distribution in the human proteome..

Intermediate Filament proteins are statistically overrepresented among human proteins identified by BackPhyre as having similarities to the C-terminal domain of Myosin II heavy chain

To evaluate whether the set of 488 proteins identified by BackPhyre is enriched with intermediate filament (IF) proteins, we performed a Fisher's exact test. We tested the null hypothesis that the 68 intermediate filament proteins within this set are a random sample from the distribution of IF proteins in the human proteome. According to UniProt (UniProt Consortium, 2024), the human proteome contains 296 IF proteins (query: "(proteome:UP000005640) AND (go:0005882)" where ‘0005882’ refers to ‘intermediate filament’ in Gene Ontology) and the number of proteins expressed by humans is 82518 (query: (proteome:UP000005640). The contingency table is thus as follows:

	Observed count	Expected count
IF	68	(296/82518)*488
Not IF	420	((82518-296)/82518)*488

That is to say:

	Observed count	Expected count
IF	68	2
Not IF	420	486

The calculated Fisher's exact p-value is 3.9359468861193E-19 (see Material and Methods). Given a significance level of 0.05, we reject the null hypothesis and conclude that intermediate filament (IF) proteins are significantly overrepresented within the set of 488 proteins identified by BackPhyre compared to their distribution in the human proteome..

Kinesins are statistically overrepresented among human proteins identified by BackPhyre as having similarities to the C-terminal domain of Myosin II heavy chain

To evaluate whether the set of 488 proteins identified by BackPhyre is enriched with kinesins, we performed a Fisher's exact test. We tested the null hypothesis that the 24 kinesins identified within this set represent a random sample from the distribution of kinesins in the human proteome. According to UniProt (UniProt Consortium, 2024), the human proteome contains 77 kinesins (query: "(proteome:UP000005640) AND (go:0005871)" where ‘0005871’ refers to ‘kinesin complex’ in Gene Ontology) and the number of proteins expressed by humans is 82518 (query: (proteome:UP000005640)). The contingency table is thus as follows:

	Observed count	Expected count
Kinesin	24	(77/82518)*488
Not kinesin	464	((82518-77)/82518)*488

That is to say:

	Observed count	Expected count
Kinesin	24	0
Not kinesin	464	488

The calculated Fisher's exact p-value is 8.9218426547255E-8 (see Material and Methods). Given a significance level of 0.05, we reject the null hypothesis and conclude that kinesins are significantly overrepresented within the set of 488 proteins identified by BackPhyre compared to their distribution in the human proteome.

Discussion

To gain deeper insights into SARS-CoV-2 infection dynamics, we re-examined the most comprehensive SARS-CoV-2–human protein interactome (Zhou *et al.*, 2022). We focused on the Spike S protein, the viral entry point that binds to the host cell receptor ACE2.

Our study leverages a protein-protein interactome derived from both Y2H (Rajagopala *et al.*, 2015) and AP-MS (Causier *et al.*, 2004), the two primary methods for large-scale interactome mapping. While these methods have limitations (see Introduction), they generally produce high-quality data. AP-MS identifies protein complexes while Y2H reveals binary interactions, providing complementary insights. Nevertheless, initially, we decided to treat Y2H and AP-MS equally as two probes of interaction. This decision was primarily driven by the observation that Human Myosin-9, identified as a Spike S partner through AP-MS in the interactome we utilized (Zhou *et al.*, 2022), had previously been demonstrated to be in close proximity to the SARS-CoV-2 Spike S protein (using an APEX2 proximity-labeling technique) and subsequently showed to directly interact with it (Chen *et al.*, 2021).

Zhou and colleagues' interactome identified 22 Spike S interactors/partners (see Material and Methods section ‘Interactome data’ and Table 1). Analysis of this set of 22 partners revealed a predominance of cytoskeleton-associated proteins, with a statistically significant overrepresentation of actin-binding proteins (10 out of 22) compared to their distribution in the human proteome (see Results sections 'Spike S partners are enriched in cytoskeleton-associated proteins, particularly actin-binding proteins', and 'Statistical analysis', and Table 2).

To further investigate the interactome results, we hypothesized that the human Spike S partners might possess a common domain mediating these interactions. Unable to identify such domains using InterPro annotations (Paysan-Lafosse *et al.*, 2022), we used Phyre2 (Kelley *et al.*, 2015) to predict the structures of the 22 Spike S partners. We then observed that 12 of these 22 structures exhibited high-confidence similarities with the tail region/domain of the Myosin II heavy chain (PDB entry 6XE9, see Results section 'A majority of Spike S partners share similarities with the C-terminal Myosin II heavy chain domain', and Table 2). Among these 12 proteins, 8 are actin-binding proteins, including human Myosin-9, which was previously shown to interact with the Spike S protein via its C-terminal domain (as mentioned in the previously).

Our analysis reveals several key findings: 1) Actin-binding proteins are significantly overrepresented among the 22 Spike S partners (10 among 22), 2) Eight of these actin-binding proteins exhibited structural similarities to the C-terminal region of Myosin II heavy chain, 3) Myosin-9, a cellular myosin and one of these eight proteins, was previously shown to interact with the Spike S protein through its C-terminal domain (Chen *et al.*, 2021). Importantly, this C-terminal domain of Myosin-9 is homologous to the C-terminal region of Myosin II heavy chain. These findings led us to hypothesize that domains homologous to the C-terminal region of Myosin II heavy chain may play a crucial role in mediating interactions with the Spike S protein.

While proteins lacking this type of domain might still interact with the Spike S protein through other, yet unidentified motifs or domains, our hypothesis provides the most parsimonious explanation for the observed data. Specifically, this hypothesis clarifies why Affinity Purification-Mass Spectrometry (AP-MS), which detects protein complexes rather than individual protein-protein interactions, might identify Spike S partners that don't exhibit similarities to the C-terminal region of Myosin II heavy chain. This is exemplified by Myosin II light chains. Myosin II light and heavy chains are integral components of the Myosin II complex. Given that the Myosin II complex binds to actin through its heavy chains, the identification of light chains by AP-MS likely reflects their association with the heavy chains within the complex, rather than indicating a direct interaction between the Spike S protein and the light chains themselves.

To identify potential human Spike S protein partners, we decided to search for human proteins sharing similarities with the C-terminal part of Myosin II heavy chain (see Results section 'The set of human proteins identified by BackPhyre is enriched in cytoskeletal-associated proteins, including actin-binding proteins, intermediate filament proteins, and kinesins'). Since this latter region is a well-known coiled-coil segment (Rahmani *et al.*, 2021), using coiled-coil prediction tools to achieve this task initially seemed relevant to us. However, a recent study surprisingly suggests that the results provided by these tools should be interpreted with caution, as evidence indicates their performance is nearly random (Simm *et al.*, 2021). This study concludes that such tools could be greatly enhanced by combining sequence profiles and secondary structure prediction. Interestingly, Phyre2 employs this approach, using PSIPRED to predict secondary structure, and integrating both alignment and secondary structure prediction into a Hidden Markov Model (see (Kelley *et al.*, 2015) for a more detailed presentation). To identify human proteins sharing similarities with the C-terminal part of Myosin II heavy chain, we thus used BackPhyre (‘Phyre2 in reverse’). Given a 3D protein structure (which inherently includes secondary structure elements), this tool searches for homologous sequences across a broad range of genomes/proteomes. We ran BackPhyre with the PDB entry 6XE9 (corresponding to the Myosin II heavy chain) to explore the human proteome (NCBI Reference Sequence Database).

BackPhyre returned 999 high-confidence hits (probability/confidence ≥ 0.97). We excluded RefSeq entries annotated as 'XP' and retained only curated RefSeq records starting with 'NP', resulting in a set of 804 well-curated RefSeq entries. We then clustered together protein isoforms, giving 622 different clusters. Next, we selected protein clusters containing at least one protein sharing similarities with the C-terminus of Myosin II heavy chain. This narrowed down the set to 488 protein clusters. Finally, each cluster was represented by a single isoform.

An initial examination of our set of 488 proteins under study (hereafter referred to as the 'focus set') revealed a significant enrichment of cytoskeletal and cytoskeleton-associated proteins. We subsequently divided this set into 7 major clusters (see Results sections ‘The set of human proteins identified by BackPhyre is enriched in cytoskeletal-associated proteins, including actin-binding proteins, intermediate filament proteins, and kinesins’ and ‘Statistical analysis’ for more details):

1./ 'Link To Actin' (67 proteins): This cluster primarily includes proteins known to interact with actin, such as actin, myosin, and tropomyosin.

2./ 'Link to Intermediate Filaments' (71 proteins): This cluster mainly includes Intermediate Filament proteins such as keratins, vimentin (known to facilitate SARS-CoV-2 entry into endothelial cells (Amraei *et al.*, 2022)), and neurofilament proteins.

3./ 'Link To Kinesin and Dynein' (46 proteins): This cluster primarily groups microtubule-based motor proteins, such as kinesins and dyneins, known to facilitate intracellular transport of various cargo like vesicles, organelles, and chromosomes. However, note that tubulins, the building blocks of microtubules, are absent from our ‘focus set’.

4./ 'Link To Microtubule' (104 proteins): This cluster encompasses proteins linked to the microtubule, including those associated with the centrosome, a vital player in various cellular processes (e.g., mitosis, where it reorganizes into the mitotic spindle, ensuring proper chromosome segregation), as well as proteins associated with cilia and flagella.

5./ 'Link To Trafficking' (51 proteins): This cluster contains, for example, several members of the BICD family. Members of this family are known to link the dynein motor complex to various cargos.

6./ 'Various Proteins' (106 proteins): This cluster includes generally small subclusters, such as the one gathering 3 proteins belonging to the LINC complex (Linker of Nucleoskeleton and Cytoskeleton), involved in the connection between the nuclear lamina and the cytoskeleton.

7./ 'Lacking UniProt Summary' (43 proteins): This cluster contains proteins lacking a UniProt 'Function' field, which was one of our main sources of information for clustering.

Importantly, we showed that our ‘focus set’ is statistically enriched not only with actin-binding proteins but also in kinesins and Intermediate Filament proteins (see ‘Statistical analysis’ subsection of Results).

Our findings are consistent with existing research emphasizing the importance of the cytoskeleton in viral infections ((Kloc *et al.*, 2022), (Wen et *al.*, 2022)): some viruses, such as HIV (Human Immunodeficiency Virus) and HPV (Human papillomavirus), use filopodia (finger-like projections on host cells), which contain bundles of actin filaments, to navigate (surf) across the cell surface and reach advantageous entry points; motor proteins subsequently assist these viruses in movement by contracting the actin filaments within filopodia; microtubules and motor proteins also play a crucial role in transporting internalized viruses to replication sites within the host cell; although the involvement of Intermediate Filaments (IFs) in viral infections is less well-understood, extracellular vimentin is an attachment factor that facilitates SARS-CoV-2 entry into human endothelial cells (Amraei *et al.*, 2022). Moreover, our identification of proteins associated with cilia (a composite structure based on microtubules (MTs) and present on the cell surface) aligns with the observed disruption of cilia function caused by coronaviruses like SARS-CoV and MERS-CoV (Wen *et al.*, 2022). Lastly, while centrosomes, which organize microtubules, are known targets for various viruses (Kodani *et al.*, 2022), there is currently no evidence for this with SARS-CoV-2. Our findings suggest this could be a promising area for further investigation.

In addition, note that the present work aligns well with our previous published study (Brézellec, 2024) where we showed that the C-terminal part of Spike S has similarities with the human prominin-1/CD133 (Weigmann *et al.*, 1997). CD133 is specific to the apical surface (the surface of a plasma membrane). It is selectively associated with microvilli (and microvilli-related structures), characterized by a dense bundle of cross-linked actin filaments that serve as their structural core. This suggests that the C-terminal part of Spike S could be involved in the delivery of virions to actin-rich regions.

Obviously, our work presents caveats that must be considered. Firstly, it's crucial to remember that the proposed interactions do not necessarily imply hijacking by the virus (some of these potential interactions might be transient and without any consequences for the host). Moreover, several factors suggest that a significant portion of the proposed interactions are improbable (e.g., potential human partners might not be expressed in the same cell type, compartment, or at the same time as the viral infection occurs, *etc.*). Consequently, a significant number of proposed interactions are likely false positives.

From a bioinformatics perspective, it is crucial to emphasize that we do not claim here that using BackPhyre to identify coiled-coil domains is a panacea. Its use is pragmatic. As mentioned previously, we employed BackPhyre as it appears to address some of the shortcomings highlighted in (Simm *et al.*, 2021). In particular, Simm *et al.* underscore that most proteins predicted to contain coiled coils do not belong to protein families with known extended coiled-coil regions, such as muscle myosins, intermediate filament proteins, and kinesins. Our results, obtained using BackPhyre, overcome this significant limitation (recall that we found that actin-binding proteins, such as myosins, IF proteins, and kinesins are statistically overrepresented). However, discussing the results described in (Simm *et al.,* 2021) or designing a method for identifying coiled-coil regions relying on BackPhyre falls outside the scope of this paper.

Despite the previously mentioned limitations, one of the main results of our work is to emphasize that Spike S might target proteins harboring coiled-coil regions, which are particularly prevalent in cytoskeletal and cytoskeleton-associated proteins (for example, myosins intermediate filament proteins, and kinesins; see (Simm *et al.*, 2021)). Further investigation is necessary to understand how this finding can deepen our knowledge of the relationship between SARS-CoV-2 and the cytoskeleton. Equally important, it will be essential in the future to evaluate whether our results are applicable to other viruses or bacteria. Indeed, it would not be surprising that viruses (and pathogenic bacteria) have evolved proteins targeting coiled-coil regions of host proteins. Some evidence already supports this hypothesis. For example, Myosin-9 promotes viral entry and infection by interacting with the envelope of several viruses, including SARS-CoV-2 as already mentioned (binding site located in the C-terminal domain (residues 1661-1960) of Myosin-9; (Chen *et al.*, 2021)) but also herpes simplex virus-1 (Arii *et al.*, 2010), Epstein-Barr virus (binding site located at 1665–1960, (Xiong *et al.*, 2015)), and Porcine Reproductive and Respiratory Syndrome Virus (binding site located at 1651–1960, (Gao *et al.*, 2016)).

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Conflict of interest disclosure

The author declares that he complies with the PCI rule of having no financial conflicts of interest in relation to the content of the article.

Supplementary information availability

Supplemental Files 1, 2, and 3 are available online (see bioRxiv, DOI of this document).

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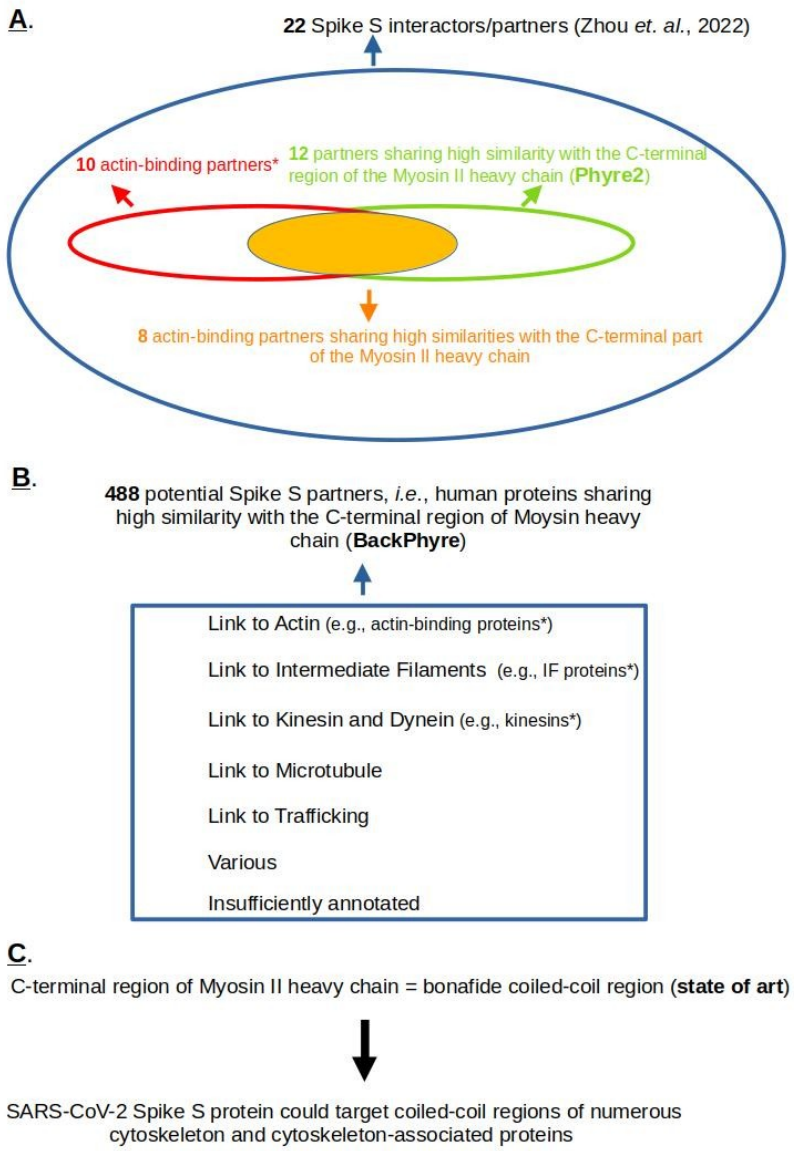

Figure - A. Focusing on a human 'Spike S interactors/partners' set of 22 proteins (Zhou *et al.*, 2022), we show that actin-binding proteins are statistically overrepresented (10 among 22) compared to their distribution in the human proteome. Next, using Phyre2 (Kelley *et al.*, 2015), a bioinformatics tool for protein structure prediction, we identify that 12 out of 22 Spike S partners contain a structural domain sharing similarities with the C-terminal part of the Myosin II heavy chain. B./ Using BackPhyre (Kelley *et al.*, 2015), a tool that identifies proteins harboring a given structural domain, we identified a set of 488 human proteins that, with high probability, share similarites with the C-terminal part of the Myosin II heavy chain. This set of proteins is particularly abundant in human cytoskeletal and associated proteins (statistically overrepresented in actin-binding proteins, Intermediate Filament proteins, and kinesins), as well as in proteins involved in microtubule dynamics. C. Given that the C-terminal domain of the Myosin II heavy chain is documented as a coiled-coil region, we infer that Spike S might target proteins containing such regions. * means statistically overrepresented.